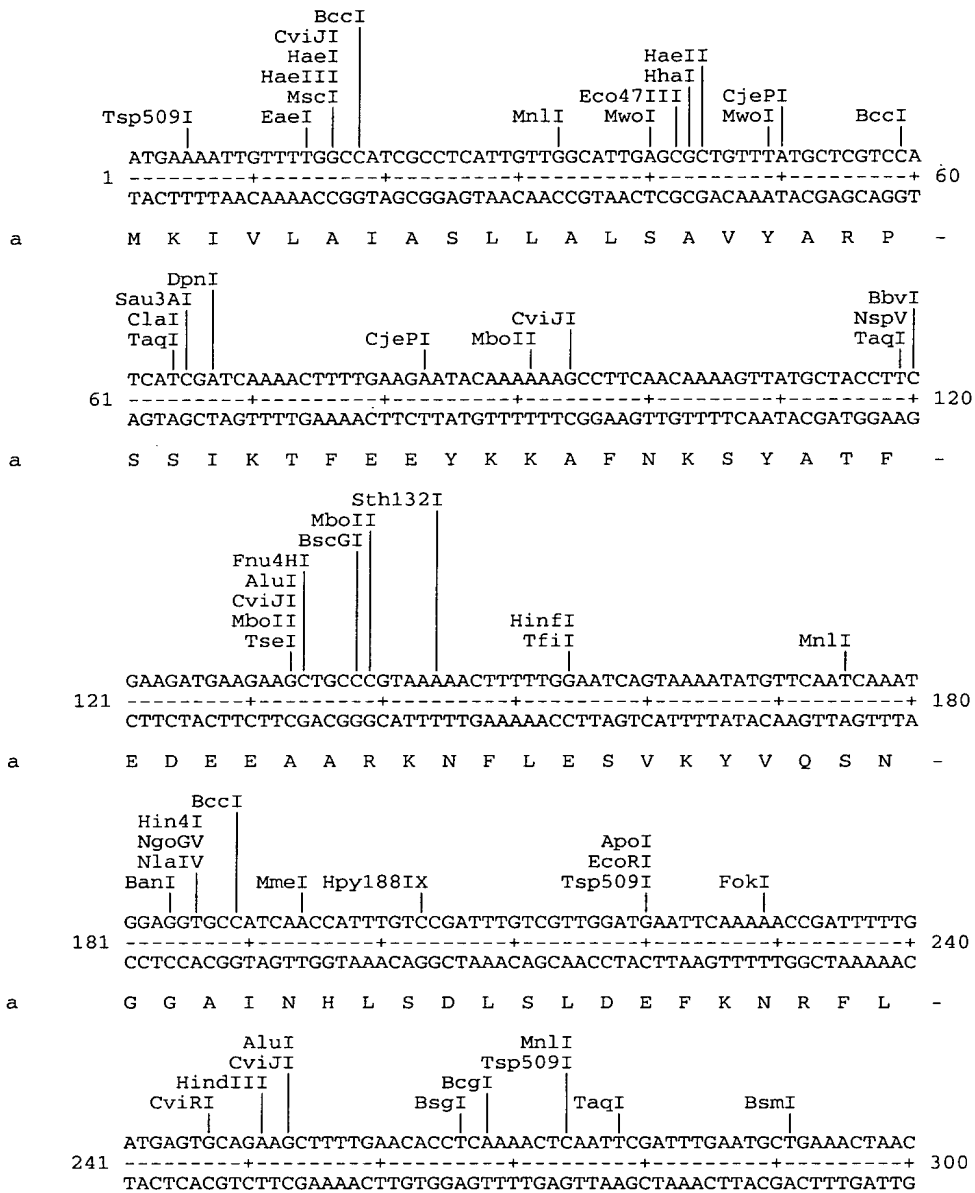




**FIGURE 7: DerP1 restriction map of SEQ ID NO. 6.**

(Linear) MAP of: Derp1.seq check: 7532 from: 1 to: 963

ID DP11695 standard; RNA; INV; 1099 BP.



a

M S A E A F E H L K T Q F D L N A E T N

BpmI  
PstI  
CviRI  
Cac8I  
SfcI  
BcgI

CjePI

AluI  
CviJI  
MspAII  
PvuII

ClaI  
TaqI

CjePI  
MwoI

MaeIII  
TaaI  
Tsp45I

BsaXI  
AloI  
PpiI

301 GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360

CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG

a A C S I N G N A P A E I D L R Q M R T V -

CviRI  
MnlI  
MslI

CviJI  
DrdII

NlaIII

CviJI

BsbI

AcII  
Fnu4HI  
TauI

361 ACTCCCATTCGTATGCAAGGAGGCTGTGGTTTCATGTTGGGCTTTCTCTGGTGTGCGCGCA 420

TGAGGGTAAGCATACGTTCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT

a T P I R M Q G G C G S C W A F S G V A A -

HinfI  
TfiI

AluI  
CviJI

CviJI  
MwoI

TaaI

BstYI  
Sau3AI

DpnI

AlwI

Tsp509I

421 ACTGAATCAGCTTATTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480

TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTCTTAAT

a T E S A Y L A Y R N Q S L D L A E Q E L -

TaqI

BsbI

TaaI

NlaIII

CjeI

MaeII

HphI

BsaAI  
FokI  
PmlI

481 GTCGATTGTGCTTCCCAACACGGTTGTTCATGGTGATACCATTCACGTTGGTATTGAATAC 540

CAGCTAACACGAAGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG

a V D C A S Q H G C H G D T I P R G I E Y -

CjeI

BstXI

MslI

AluI  
CviJI  
MmeI

ClaI  
TaqI

MaeII

BssSI  
CviRI

541 ATCCAACATAATGGTGTCTGCTCCAAGAAAGCTACTATCGATACGTTGCACGAGAACATCA 600

TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT

a I Q H N G V V Q E S Y Y R Y V A R E Q S -

NlaIII

CviRI

AcII  
MaeII

ApoI  
Tsp509I  
CjeI

601 TGCCGACGACCAATGCACAACGTTTCGGTATCTCAAATATTGCCAAATTTACCCACCA 660

ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT

a C R R P N A Q R F G I S N Y C Q I Y P P -

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AluI  
CviJI  
CjeI  
HindIII  
Hpy178III  
ApoI  
Tsp509I  
CviJI  
BceI  
Eco47III  
HaeII  
HhaI  
RleAI

661 AATGTAACAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720  
-----+-----+-----+-----+-----+  
TTACATTGTGTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA

a N V N K I R E A L A Q T H S A I A V I I -

CviJI  
HaeIII  
BccI  
EaeI  
GdiII  
SfaNI  
BsmI  
HgaI  
MslI  
ThaI

721 GGCATCAAGATTTAGACGATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780  
-----+-----+-----+-----+-----+  
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA

a G I K D L D A F R H Y D G R T I I Q R D -

BstEII  
MaeIII  
HincII  
MaeIII  
TaaI  
DraIII

781 AATGGTTACCAACCAAACTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840  
-----+-----+-----+-----+-----+  
TTACCAATGGTTGGTTTGATAGTGCACAGTTGTAACAACCAATGTTCATTGCGTGTTCCA

a N G Y Q P N Y H A V N I V G Y S N A Q G -

CjeI  
TaaI  
BciVI  
CjePI  
AlwI  
RsaI  
SunI  
DpnI  
Sau3AI  
TaqI  
HgiEII  
MunI  
Tsp509I  
MaeIII  
CjePI  
HphI  
BbvI  
TaaI  
CjeI

841 GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900  
-----+-----+-----+-----+-----+  
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA

a V D Y W I V R N S W D T N W G D N G Y G -

Fnu4HI  
TseI  
ClaI  
TaqI  
Bsp24I  
CjePI  
CjeI  
MboII  
NdeI

901 TATTTTGCTGCCAACATCGATTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960  
-----+-----+-----+-----+-----+  
ATAAAACGACGGTTGTAGCTAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG

a Y F A A N I D L M M I E E Y P Y V V I L -

TAA  
961 --- 963  
ATT

**FIGURE 8:** Sequence of full mutant DerP1 including pre-protein. Active site mutation Cys 132→Ala 132, corresponding to Cys34→Ala34 of the mature protein). Sequence includes coding (listed as SEQ ID NO. [[5]]6) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. [[6]]1).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTTGGAATCAGTAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTGAATGCTGAAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTTGTTGGAGTTTTGAGTTAAGCTAAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCAGCTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTCGAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S A W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG  
V D C A S Q H G C H G D T I P R G I E Y 180  
  
ATCCAACATAATGGTGTCTGTCCTCAAGAAAGCTACTATCGATACGTTGCACGAGAACAAATCA 600  
-----+-----+-----+-----+-----+-----+-----+  
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT  
I Q H N G V V Q E S Y Y R Y V A R E Q S 200  
  
TGCCGACGACCAAATGCACAACGTTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660  
-----+-----+-----+-----+-----+-----+-----+  
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT  
C R R P N A Q R F G I S N Y C Q I Y P P 220  
  
AATGTAAACAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720  
-----+-----+-----+-----+-----+-----+-----+  
TTACATTTGTTTTAAGCACTTCGAAACCGAGTTTGGGTGTCGCGATAACGGCAGTAATAA  
N V N K I R E A L A Q T H S A I A V I I 240  
  
GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780  
-----+-----+-----+-----+-----+-----+-----+  
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA  
G I K D L D A F R H Y D G R T I I Q R D 260  
  
AATGGTTACCAACCAAACCTATCACGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840  
-----+-----+-----+-----+-----+-----+-----+  
TTACCAATGGTTGGTTTGATAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA  
N G Y Q P N Y H A V N I V G Y S N A Q G 280  
  
GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAATAACCTAGCATGCTTTGTCAACCCTATGGTTAACCCCACTATTACCAATGCCA  
V D Y W I V R N S W D T N W G D N G Y G 300  
  
TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960  
-----+-----+-----+-----+-----+-----+-----+  
ATAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG  
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

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ATT

**FIGURE 9:** Sequence of full mutant DerP1 including pre-protein containing a deletion at the propeptide cleavage site (NAET). Sequence includes coding (listed as SEQ ID NO. [[1]]7) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. 2).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACCTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTTGGAATCAGTAAAAATATGTTCAATCAAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTG AAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCCTTCGAAAACCTGTGGAGTTTGTAGTTAAGCTAAAC TTG
M S A E A F E H L K T Q F D L N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTTGCCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCTCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG  
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAATCA 600  
-----+-----+-----+-----+-----+-----+-----+  
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT  
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660  
-----+-----+-----+-----+-----+-----+-----+  
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT  
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720  
-----+-----+-----+-----+-----+-----+-----+  
TTACATTTGTTTAAAGCACTTCGAAACCGAGTTTGGGTGTTCGCGATAACGGCAGTAATAA  
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780  
-----+-----+-----+-----+-----+-----+-----+  
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA  
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACTATGCTGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840  
-----+-----+-----+-----+-----+-----+-----+  
TTACCAATGGTTGGTTTGTAGTGCGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA  
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAATAACCTAGCATGCTTTGTCAACCCCTATGGTTAACCCCACTATTACCAATGCCA  
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960  
-----+-----+-----+-----+-----+-----+-----+  
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG  
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA  
---  
ATT

**FIGURE 10:** Sequence of full mutant DerP1 including pre-protein. Active site mutation His 268 → Ala 268, corresponding to His170→Ala170 of the mature protein). Sequence includes coding (listed as SEQ ID NO. [[3]]8) and complementary DNA, and amino acid sequences (listed as SEQ ID NO. [[4]]3).

```
ATGAAAATTGTTTTGGCCATCGCCTCATTGTTGGCATTGAGCGCTGTTTATGCTCGTCCA 60
-----+-----+-----+-----+-----+-----+
TACTTTTAACAAAACCGGTAGCGGAGTAACAACCGTAACTCGCGACAAATACGAGCAGGT
M K I V L A I A S L L A L S A V Y A R P 20

TCATCGATCAAACTTTTGAAGAATACAAAAAGCCTTCAACAAAAGTTATGCTACCTTC 120
-----+-----+-----+-----+-----+-----+
AGTAGCTAGTTTTGAAAACCTTCTTATGTTTTTCGGAAGTTGTTTTCAATACGATGGAAG
S S I K T F E E Y K K A F N K S Y A T F 40

GAAGATGAAGAAGCTGCCCCGTAAAACTTTTTGGAATCAGTAAAATATGTTCAATCAAAT 180
-----+-----+-----+-----+-----+-----+
CTTCTACTTCTTCGACGGGCATTTTTGAAAACCTTAGTCATTTTATACAAGTTAGTTTA
E D E E A A R K N F L E S V K Y V Q S N 60

GGAGGTGCCATCAACCATTTGTCCGATTTGTCGTTGGATGAATTCAAAAACCGATTTTTTG 240
-----+-----+-----+-----+-----+-----+
CCTCCACGGTAGTTGGTAAACAGGCTAAACAGCAACCTACTTAAGTTTTTGGCTAAAAAC
G G A I N H L S D L S L D E F K N R F L 80

ATGAGTGCAGAAGCTTTTGAACACCTCAAACTCAATTCGATTTGAATGCTGAAACTAAC 300
-----+-----+-----+-----+-----+-----+
TACTCACGTCTTCGAAAACCTTGTTGGAGTTTTGAGTTAAGCTAAACTTACGACTTTGATTG
M S A E A F E H L K T Q F D L N A E T N 100

GCCTGCAGTATCAATGGAAATGCTCCAGCTGAAATCGATTTGCGACAAATGCGAACTGTC 360
-----+-----+-----+-----+-----+-----+
CGGACGTCATAGTTACCTTTACGAGGTCGACTTTAGCTAAACGCTGTTTACGCTTGACAG
A C S I N G N A P A E I D L R Q M R T V 120

ACTCCCATTTCGTATGCAAGGAGGCTGTGGTTCATGTTGGGCTTTCTCTGGTGTGCGCA 420
-----+-----+-----+-----+-----+-----+
TGAGGGTAAGCATACGTTCCCTCCGACACCAAGTACAACCCGAAAGAGACCACAACGGCGT
T P I R M Q G G C G S C W A F S G V A A 140

ACTGAATCAGCTTATTTGGCTTACCGTAATCAATCATTGGATCTTGCTGAACAAGAATTA 480
-----+-----+-----+-----+-----+-----+
TGACTTAGTCGAATAAACCGAATGGCATTAGTTAGTAACCTAGAACGACTTGTTCTTAAT
T E S A Y L A Y R N Q S L D L A E Q E L 160
```



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GTCGATTGTGCTTCCCAACACGGTTGTCATGGTGATACCATTCCACGTGGTATTGAATAC 540  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAACACGAAGGGTTGTGCCAACAGTACCACTATGGTAAGGTGCACCATAACTTATG  
V D C A S Q H G C H G D T I P R G I E Y 180

ATCCAACATAATGGTGTCTGCCAAGAAAGCTACTATCGATACGTTGCACGAGAACAATCA 600  
-----+-----+-----+-----+-----+-----+-----+  
TAGGTTGTATTACCACAGCAGGTTCTTTTCGATGATAGCTATGCAACGTGCTCTTGTTAGT  
I Q H N G V V Q E S Y Y R Y V A R E Q S 200

TGCCGACGACCAAATGCACAACGTTTCGGTATCTCAAACCTATTGCCAAATTTACCCACCA 660  
-----+-----+-----+-----+-----+-----+-----+  
ACGGCTGCTGGTTTACGTGTTGCAAAGCCATAGAGTTTGATAACGGTTTAAATGGGTGGT  
C R R P N A Q R F G I S N Y C Q I Y P P 220

AATGTAAACAAAATTCGTGAAGCTTTGGCTCAAACCCACAGCGCTATTGCCGTCATTATT 720  
-----+-----+-----+-----+-----+-----+-----+  
TTACATTTGTTTAAAGCACTTCGAAACCGAGTTTGGGTGTGCGGATAACGGCAGTAATAA  
N V N K I R E A L A Q T H S A I A V I I 240

GGCATCAAAGATTTAGACGCATTCCGTCATTATGATGGCCGAACAATCATTCAACGCGAT 780  
-----+-----+-----+-----+-----+-----+-----+  
CCGTAGTTTCTAAATCTGCGTAAGGCAGTAATACTACCGGCTTGTTAGTAAGTTGCGCTA  
G I K D L D A F R H Y D G R T I I Q R D 260

AATGGTTACCAACCAAACCTATGCTGCTGTCAACATTGTTGGTTACAGTAACGCACAAGGT 840  
-----+-----+-----+-----+-----+-----+-----+  
TTACCAATGGTTGGTTTGATACGACGACAGTTGTAACAACCAATGTCATTGCGTGTTCCA  
N G Y Q P N Y A A V N I V G Y S N A Q G 280

GTCGATTATTGGATCGTACGAAACAGTTGGGATACCAATTGGGGTGATAATGGTTACGGT 900  
-----+-----+-----+-----+-----+-----+-----+  
CAGCTAATAACCTAGCATGCTTTGTCAACCCCTATGGTTAACCCCACTATTACCAATGCCA  
V D Y W I V R N S W D T N W G D N G Y G 300

TATTTTGCTGCCAACATCGATTTGATGATGATTGAAGAATATCCATATGTTGTCATTCTC 960  
-----+-----+-----+-----+-----+-----+-----+  
ATAAAACGACGGTTGTAGCTAAACTACTACTAACTTCTTATAGGTATACAACAGTAAGAG  
Y F A A N I D L M M I E E Y P Y V V I L 320

TAA

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ATT

**FIGURE 11:** Amino acid sequence (SEQ ID NO: [[7]]4) for the mutant DerP1 as encoded by pNIV4842, and shown in figure 5.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE  
51 EYKKAFNKS Y ATFEDDEEAAR KNFLESVKYV QSNNGGAINHL SDLSLDEFKN  
101 RFLMSAEAFE HLKTQFDLNA CSINGNAPAE IDLRQMRTVT PIRMQGGCGS  
151 CWA FSGVAAT ESAYLAYRNQ SLDLAEQELV DCASQHGCHG DTIPRGIEYI  
201 QHNGVVQESY YRYVAREQSC RRPNAQRFGI SNYCQIYPPN ANKIREALAQ  
251 THSAIAVIIG IKDLDAFRHY DGRTIIQRDN GYQPNYHAVN IVGYSNAQGV  
301 DYWIVRNSWD TNWGDNGYGY FAANIDLMMI EEYPYVVIL\*



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**FIGURE 12:** Amino acid sequence (SEQ ID NO: [[8]]5) for the mutant DerP1 as encoded by pNIV4843, and shown in figure 6.

1 MLLVNQSHQG FNKEHTSKMV SAIVLYVLLA AAAHSAFAAD PRPSSIKTFE  
51 EYKKA FNKSY ATFEDEEAAR KNFLESVKYV QSNGGAINHL SDLSLDEFKN  
101 RFLMSAEAFE HLKTQFDLNA ETNACSINGN APAEIDLRQM RTVTPIRMQG  
151 GCGSAWAFSG VAATESAYLA YRNQSLDLAE QELVDCASQH GCHGDTIPRG  
201 IEYIQHNGVV QESYYRYVAR EQSCRRPNAQ RFGISNYCQI YPPNANKIRE  
251 ALAQTHSAIA VIIGIKDLDA FRHYDGRTII QRDNGYQPNY HAVNIVGYSN  
301 AQGVVDYWIVR NSWDTNWGDN GYGYFAANID LMMIEEYPYV VIL\*